

SEQUENCE LISTING

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<120> USE OF PROTEINS AND PEPTIDES CODED BY THE GENOME OF A NOVEL STRAIN OF
SARS-ASSOCIATED CORONAVIRUS

<130> 226-111ext

<150> FR 0314152
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<170> PatentIn version 3.1

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 240 245 250

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 Leu Cys Trp Lys Cys Lys Ser Lys Asn Pro Leu Leu Tyr Asp Ala Asn
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tcttgctttg ttgcatgact agttgttgca gttgcctcaa ggggtgcatgc tcttggtggtt      60
cttgctgcaa gtttgatgag gatgactctg agccagttct caaggggtgtc aaattacatt      120
acacataaac gaacttatgg atttgtttat gagatttttt actccttggtat caattactgc      180
acagccagta aaaattgaca atgcttctcc tgcaagtact gttcatgcta cagcaacgat      240
accgctacaa gcctcactcc ctttcggatg gcttggtatt ggcgttgcat ttcttgctgt      300
ttttcagagc gctacccaaa taattgctgct caataaaaga tggcagctag ccctttataa      360
gggcttccag ttcatttgca atttactgct gctatttggt accatctatt cacatctttt      420
gcttgctgct gcaggatgg aggcgcaatt tttgtacctc tatgccttga tatattttct      480
acaatgcac aacgcagta gaattattat gagatgttgg ctttggttga agtgcaaadc      540
caagaaccca ttacttt atg atg cca act act ttg ttt gct ggc aca cac      590
Met Met Pro Thr Thr Leu Phe Ala Gly Thr His
1 5 10
ata act atg act act gta tac cat ata aca gtg tca cag ata caa ttg      638
Ile Thr Met Thr Thr Val Tyr His Ile Thr Val Ser Gln Ile Gln Leu
15 20 25
tcg tta ctg aag gtg acg gca ttt caa cac caa aac tca aag aag act      686
Ser Leu Leu Lys Val Thr Ala Phe Gln His Gln Asn Ser Lys Lys Thr
30 35 40
acc aaa ttg gtg gtt att ctg agg ata ggc act cag gtg tta aag act      734
Thr Lys Leu Val Val Ile Leu Arg Ile Gly Thr Gln Val Leu Lys Thr
45 50 55
atg tcg ttg tac atg gct att tca ccg aag ttt act acc agc ttg agt      782
Met Ser Leu Tyr Met Ala Ile Ser Pro Lys Phe Thr Thr Ser Leu Ser
60 65 70 75
cta cac aaa tta cta cag aca ctg gta ttg aaa atg cta cat tct tca      830
Leu His Lys Leu Gln Thr Leu Val Leu Lys Met Leu His Ser Ser
80 85 90
tct tta aca agc ttg tta aag acc cac cga atg tgc aaa tac aca caa      878
Ser Leu Thr Ser Leu Leu Lys Thr His Arg Met Cys Lys Tyr Thr Gln
95 100 105
tcg acg gct ctt cag gag ttg cta atc cag caa tgg atc caa ttt atg      926
Ser Thr Ala Leu Gln Glu Leu Leu Ile Gln Gln Trp Ile Gln Phe Met
110 115 120
atg agc cga cga cga cta cta gcg tgc ctt tgt aag cac aag aaa gtg      974
Met Ser Arg Arg Arg Leu Leu Ala Cys Leu Cys Lys His Lys Lys Val
125 130 135
agt acg aac tta tgt act cat tcg ttt cgg aag aaa cag gta cgt      1019
Ser Thr Asn Leu Cys Thr His Ser Phe Arg Lys Lys Gln Val Arg
140 145 150
taatagttaa tagcgactt ctttttcttg ctttcgtggg attccttgcta gtcacactag      1079
ccatccttac tgcgctt      1096

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<210> 12
 <211> 154
 <212> PRT
 <213> CORONAVIRUS

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<400> 12
Met Met Pro Thr Thr Leu Phe Ala Gly Thr His Ile Thr Met Thr Thr
1 5 10 15
Val Tyr His Ile Thr Val Ser Gln Ile Gln Leu Ser Leu Lys Val
20 25 30
Thr Ala Phe Gln His Gln Asn Ser Lys Lys Thr Thr Lys Leu Val Val
35 40 45
Ile Leu Arg Ile Gly Thr Gln Val Leu Lys Thr Met Ser Leu Tyr Met
50 55 60
Ala Ile Ser Pro Lys Phe Thr Thr Ser Leu Ser Leu His Lys Leu Leu
65 70 75 80
Gln Thr Leu Val Leu Lys Met Leu His Ser Ser Ser Leu Thr Ser Leu
85 90 95
Leu Lys Thr His Arg Met Cys Lys Tyr Thr Gln Ser Thr Ala Leu Gln
100 105 110

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Glu Leu Leu Ile Gln Gln Trp Ile Gln Phe Met Met Ser Arg Arg Arg
 115 120 125
 Leu Leu Ala Cys Leu Cys Lys His Lys Lys Val Ser Thr Asn Leu Cys
 130 135 140
 Thr His Ser Phe Arg Lys Lys Gln Val Arg
 145 150

<210> 13
 <211> 332
 <212> DNA
 <213> CORONAVIRUS

<220>
 <221> CDS
 <222> (36)..(263)
 <223>

<400> 13
 tgcctttgta agcacaagaa agtgagtacg aactt atg tac tca ttc gtt tcg 53
 Met Tyr Ser Phe Val Ser
 1 5
 gaa gaa aca ggt acg tta ata gtt aat agc gta ctt ctt ttt ctt gct 101
 Glu Glu Thr Gly Thr Leu Ile Val Asn Ser Val Leu Leu Phe Leu Ala
 10 15 20
 ttc gtg gta ttc ttg cta gtc aca cta gcc atc ctt act gcg ctt cga 149
 Phe Val Val Phe Leu Leu Val Thr Leu Ala Ile Leu Thr Ala Leu Arg
 25 30 35
 ttg tgt gcg tac tgc tgc aat att gtt aac gtg agt tta gta aaa cca 197
 Leu Cys Ala Tyr Cys Cys Asn Ile Val Asn Val Ser Leu Val Lys Pro
 40 45 50
 acg gtt tac gtc tac tcg cgt gtt aaa aat ctg aac tct tct gaa gga 245
 Thr Val Tyr Val Tyr Ser Arg Val Lys Asn Leu Asn Ser Ser Glu Gly
 55 60 65 70
 gtt cct gat ctt ctg gtc taaacgaact aactattatt attattctgt 293
 Val Pro Asp Leu Leu Val
 75
 ttggaacttt aacattgctt atcatggcag acaacggta 332

<210> 14
 <211> 76
 <212> PRT
 <213> CORONAVIRUS

<400> 14
 Met Tyr Ser Phe Val Ser Glu Glu Thr Gly Thr Leu Ile Val Asn Ser
 1 5 10 15
 Val Leu Leu Phe Leu Ala Phe Val Val Phe Leu Leu Val Thr Leu Ala
 20 25 30
 Ile Leu Thr Ala Leu Arg Leu Cys Ala Tyr Cys Cys Asn Ile Val Asn
 35 40 45
 Val Ser Leu Val Lys Pro Thr Val Tyr Val Tyr Ser Arg Val Lys Asn
 50 55 60
 Leu Asn Ser Ser Glu Gly Val Pro Asp Leu Leu Val
 65 70 75

<210> 15
 <211> 332
 <212> DNA
 <213> CORONAVIRUS

<400> 15
 tgcctttgta agcacaagaa agtgagtacg aacttatgta ctcattcgtt tcggaagaaa 60

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caggtacggt aatagttaat agcgtacttc tttttcttgc tttcgtggta ttcttgctag 120
tcacactagc catccttact gcgcttcgat tgtgtgcgta ctgctgcaat attgttaacg 180
tgagtttagt aaaaccaacg gtttacgtct actcgcgtgt taaaaatctg aactcttctg 240
aaggagttcc tgatcttctg gtctaaacga actaactatt attattattc tgtttggaac 300
ttaacattg cttatcatgg cagacaacgg ta 332

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<210> 16
<211> 708
<212> DNA
<213> CORONAVIRUS

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<220>
<221> CDS
<222> (41)..(703)
<223>

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<400> 16
tattattatt attctgtttg gaactttaac attgcttatt atg gca gac aac ggt 55
Met Ala Asp Asn Gly
1 5
act att acc gtt gag gag ctt aaa caa ctc ctg gaa caa tgg aac cta 103
Thr Ile Thr Val Glu Glu Leu Lys Gln Leu Leu Glu Gln Trp Asn Leu
10 15 20
gta ata ggt ttc cta ttc cta gcc tgg att atg tta cta caa ttt gcc 151
Val Ile Gly Phe Leu Phe Leu Ala Trp Ile Met Leu Leu Gln Phe Ala
25 30 35
tat tct aat cgg aac agg ttt ttg tac ata ata aag ctt gtt ttc ctc 199
Tyr Ser Asn Arg Asn Arg Phe Leu Tyr Ile Ile Lys Leu Val Phe Leu
40 45 50
tgg ctc ttg tgg cca gta aca ctt gct tgt ttt gtg ctt gct gct gtc 247
Trp Leu Leu Trp Pro Val Thr Leu Ala Cys Phe Val Leu Ala Ala Val
55 60 65
tac aga att aat tgg gtg act ggc ggg att gcg att gca atg gct tgt 295
Tyr Arg Ile Asn Trp Val Thr Gly Gly Ile Ala Ile Ala Met Ala Cys
70 75 80 85
att gta ggc ttg atg tgg ctt agc tac ttc gtt gct tcc ttc agg ctg 343
Ile Val Gly Leu Met Trp Leu Ser Tyr Phe Val Ala Ser Phe Arg Leu
90 95 100
ttt gct cgt acc cgc tca atg tgg tca ttc aac cca gaa aca aac att 391
Phe Ala Arg Thr Arg Ser Met Trp Ser Phe Asn Pro Glu Thr Asn Ile
105 110 115
ctt ctc aat gtg cct ctc cgg ggg aca att gtg acc aga ccg ctc atg 439
Leu Leu Asn Val Pro Leu Arg Gly Thr Ile Val Thr Arg Pro Leu Met
120 125 130
gaa agt gaa ctt gtc att ggt gct gtg atc att cgt ggt cac ttg cga 487
Glu Ser Glu Leu Val Ile Gly Ala Val Ile Ile Arg Gly His Leu Arg
135 140 145
atg gcc gga cac tcc cta ggg cgc tgt gac att aag gac ctg cca aaa 535
Met Ala Gly His Ser Leu Gly Arg Cys Asp Ile Lys Asp Leu Pro Lys
150 155 160 165
gag atc act gtg gct aca tca cga acg ctt tct tat tac aaa tta gga 583
Glu Ile Thr Val Ala Thr Ser Arg Thr Leu Ser Tyr Tyr Lys Leu Gly
170 175 180
gcg tcg cag cgt gta ggc act gat tca ggt ttt gct gca tac aac cgc 631
Ala Ser Gln Arg Val Gly Thr Asp Ser Gly Phe Ala Ala Tyr Asn Arg
185 190 195
tac cgt att gga aac tat aaa tta aat aca gac cac gcc ggt agc aac 679
Tyr Arg Ile Gly Asn Tyr Lys Leu Asn Thr Asp His Ala Gly Ser Asn
200 205 210
gac aat att gct ttg cta gta cag taagt 708
Asp Asn Ile Ala Leu Leu Val Gln
215 220

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<210> 17
 <211> 221
 <212> PRT
 <213> CORONAVIRUS

<400> 17
 Met Ala Asp Asn Gly Thr Ile Thr Val Glu Glu Leu Lys Gln Leu Leu
 1 5 10 15
 Glu Gln Trp Asn Leu Val Ile Gly Phe Leu Phe Leu Ala Trp Ile Met
 20 25 30
 Leu Leu Gln Phe Ala Tyr Ser Asn Arg Asn Arg Phe Leu Tyr Ile Ile
 35 40 45
 Lys Leu Val Phe Leu Trp Leu Leu Trp Pro Val Thr Leu Ala Cys Phe
 50 55 60
 Val Leu Ala Ala Val Tyr Arg Ile Asn Trp Val Thr Gly Gly Ile Ala
 65 70 75 80
 Ile Ala Met Ala Cys Ile Val Gly Leu Met Trp Leu Ser Tyr Phe Val
 85 90 95
 Ala Ser Phe Arg Leu Phe Ala Arg Thr Arg Ser Met Trp Ser Phe Asn
 100 105 110
 Pro Glu Thr Asn Ile Leu Leu Asn Val Pro Leu Arg Gly Thr Ile Val
 115 120 125
 Thr Arg Pro Leu Met Glu Ser Glu Leu Val Ile Gly Ala Val Ile Ile
 130 135 140
 Arg Gly His Leu Arg Met Ala Gly His Ser Leu Gly Arg Cys Asp Ile
 145 150 155 160
 Lys Asp Leu Pro Lys Glu Ile Thr Val Ala Thr Ser Arg Thr Leu Ser
 165 170 175
 Tyr Tyr Lys Leu Gly Ala Ser Gln Arg Val Gly Thr Asp Ser Gly Phe
 180 185 190
 Ala Ala Tyr Asn Arg Tyr Arg Ile Gly Asn Tyr Lys Leu Asn Thr Asp
 195 200 205
 His Ala Gly Ser Asn Asp Asn Ile Ala Leu Leu Val Gln
 210 215 220

<210> 18
 <211> 769
 <212> DNA
 <213> CORONAVIRUS

<400> 18
 cctgatcttc tgggtctaaac gaactaacta ttattattat tctgtttgga actttaacat 60
 tgcttatcat ggcagacaac ggtactatta ccgttgagga gcttaaaca ctcctggaac 120
 aatggaacct agtaataggt ttcctattcc tagcctggat tatgttacta caatttgcct 180
 attctaatacg gaacagggtt ttgtacataa taaagcttgt tttcctctgg ctcttggtggc 240
 cagtaacact tgcttggttt gtgcttgctg ctgtctacag aattaattgg gtgactggcg 300
 ggattgcat tgcaatggct tgtattgtag gcttgatgtg gcttagctac ttcgttgctt 360
 ccttcaggct gtttgctcgt acccgctcaa tgtggctcatt caaccagaa acaaacattc 420
 ttctcaatgt gcctctccgg gggacaattg tgaccagacc gctcatggaa agtgaacttg 480
 tcattggtgc tgtgatcatt cgtggctcact tgcaatggc cggacactcc ctaggggcgt 540
 gtgacattaa ggacctgcca aaagagatca ctgtggctac atcacgaacg ctttcttatt 600
 acaaattagg agcgtcgag cgtgtaggca ctgattcagg ttttgctgca tacaaccgct 660
 accgtattgg aaactataaa ttaaatacag accacgccgg tagcaacgac aatattgctt 720
 tgctagtaca gtaagtgaca acagatgttt catcttggtg acttcagg 769

<210> 19
 <211> 1231
 <212> DNA
 <213> CORONAVIRUS

<400> 19
 taccgtattg gaaactataa attaaataga gaccacgccg gtagcaacga caatattgct 60

ttgctagtag	acgtaagtgc	aacagatggt	tcattcttgt	gacttccagg	ttacaatagc	120
agagatat	attatcatta	tgaggacttt	caggattgct	atttggaatc	ttgacgttat	180
aataagttca	atagtgcagc	aattatttta	gcctctaact	aagaagaatt	attcggagtt	240
agatgatgaa	gaacctatgg	agttagatta	tccataaaac	gaacatgaaa	attattctct	300
tcctgacatt	gattgtattt	acatcttgcg	agctatatca	ctatcaggag	tgtgttagag	360
gtacgactgt	actactaaaa	gaaccttgcc	catcaggaac	atacgagggc	aattcaccat	420
ttcacctct	tgctgacaat	aaatttgcac	taacttgcac	tagcacacac	tttgcttttg	480
cttggtgctga	cggtagctga	catacctatc	agctgcgtgc	aagatcagtt	tcacccaaaac	540
ttttcatcag	acaagaggag	gttcaacaag	agctctactc	gccacttttt	ctcattgttg	600
ctgctctagt	atttttaata	ctttgcttca	ccattaagag	aaagacagaa	tgaatgagct	660
cactttaatt	gacttctatt	tgtgcttttt	agcctttctg	ctattccttg	ttttaataat	720
gcttattata	ttttgggttt	cactcgaaat	ccaggatcta	gaagaacctt	gtacccaaagt	780
ctaaacgaac	atgaaacttc	tcattgtttt	gacttgtatt	tctctatgca	gttgcatatg	840
cactgtagta	cagcgctgtg	catctaataa	acctcatgtg	cttgaagatc	cttgtaagggt	900
acaacactag	gggtaatact	tatagcactg	cttggtcttg	tgctctagga	aagggtttac	960
cttttcatag	atggcacact	atggttcaaa	catgcacacc	taatgttact	atcaactgtc	1020
aagatccagc	tggtgggtgc	cttatagcta	ggtgttggtg	ccttcatgaa	ggtcacccaaa	1080
ctgctgcatt	tagagacgta	cttggtgttt	taaataaacg	aacaaattaa	aatgtctgat	1140
aatggacccc	aatcaaacca	acgtagtgc	ccccgcatta	catttggtgg	acccacagat	1200
tcaactgaca	ataaccagaa	tggaggacgc	a			1231

<210> 20
 <211> 1242
 <212> DNA
 <213> CORONAVIRUS

<400> 20						
gcatacaacc	gctaccgtat	tggaaactat	aaattaaata	cagaccacgc	cggtagcaac	60
gacaatattg	ctttgctagt	acagtaagtg	acaacagatg	tttcatcttg	ttgacttcca	120
ggttacaata	gcagagatat	tgattatcat	tatgaggact	ttcaggattg	ctatttgga	180
tcttgacgtt	ataataagtt	caatagtgcg	acagttattt	aagcctctaa	ctaagaagaa	240
ttattcggag	ttagatgatg	aagaacctat	ggagttagat	tatccataaa	acgaacatga	300
aaattattct	cttcctgaca	ttgattgtat	ttacatcttg	cgagctatat	cactatcagg	360
agtgtgttag	aggtacgact	gtactactaa	aagaaccttg	cccatcagga	acatacaggg	420
gcaattcacc	atttcaccct	cttgctgaca	ataaatttgc	actaacttgc	actagcacac	480
actttgcttt	tgcttgctgt	gacggtagtc	gacataccta	tcagctgcgt	gcaagatcag	540
tttcacccaa	acttttcatc	agacaagagg	aggttcaaca	agagctctac	tcgccacttt	600
ttctcattgt	tgctgctcta	gtatttttta	tactttgctt	caccattaag	agaaagacag	660
aatgaatgag	ctcactttta	ttgacttcta	tttgctgctt	ttagcctttc	tgctattcct	720
tgtttttaata	atgcttatta	tattttgggt	ttcactcgaa	atccaggatc	tagaagaacc	780
ttgtacccaa	gtctaaacga	acatgaaact	tctcattgtt	ttgacttgta	tttctctatg	840
cagttgcata	tgcaactgtg	tacagcgctg	tgcatcta	aaacctcatg	tgcttgaaga	900
tccttgtaag	gtacaacact	aggggttaata	cttatagcac	tgcttggctt	tgtgctctag	960
gaaagggttt	accttttcat	agatggcaca	ctatgggttca	aacatgcaca	cctaattgtta	1020
ctatcaactg	tcaagatcca	gctgggtggtg	cgcttatagc	taggtgttgg	taccttcatg	1080
aaggtcacca	aactgctgca	tttagagacg	tacttgttgt	tttaataaaa	cgaacgaatt	1140
aaaatgtctg	ataatggacc	ccaatcaaac	caacgtagtg	ccccccgc	tacatttggt	1200
ggacccacag	attcaactga	caataaccag	aatggaggac	gc		1242

<210> 21
 <211> 1231
 <212> DNA
 <213> CORONAVIRUS

<220>						
<221> CDS						
<222> (86) .. (274)						
<223>						
<400> 21						
taccgtattg	gaaactataa	attaaataca	gaccacgccg	gtagcaacga	caatattgct	60

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ttgctagtagtac agtaagtgac aacag atg ttt cat ctt gtt gac ttc cag gtt      112
                               Met Phe His Leu Val Asp Phe Gln Val
                               1       5
aca ata gca gag ata ttg att atc att atg agg act ttc agg att gct      160
Thr Ile Ala Glu Ile Leu Ile Ile Ile Met Arg Thr Phe Arg Ile Ala
10       15       20       25
att tgg aat ctt gac gtt ata ata agt tca ata gtg aga caa tta ttt      208
Ile Trp Asn Leu Asp Val Ile Ile Ser Ser Ile Val Arg Gln Leu Phe
       30       35       40
aag cct cta act aag aag aat tat tgc gag tta gat gat gaa gaa cct      256
Lys Pro Leu Thr Lys Lys Asn Tyr Ser Glu Leu Asp Asp Glu Glu Pro
       45       50       55
atg gag tta gat tat cca taaaacgaac atgaaaatta ttctcttcct      304
Met Glu Leu Asp Tyr Pro
       60
gacattgatt gtatttacat cttgcgagct atatcactat caggagtggtg ttagaggtac      364
gactgtacta ctaaaagaac cttgcccac aggaacatac gagggcaatt caccatttca      424
ccctcttgct gacaataaat ttgcactaac ttgcactagc acacactttg cttttgcttg      484
tgctgacggg actcgacata cctatcagct gcgtgcaaga tcagtttcac caaaactttt      544
catcagacaa gaggagggtt aacaagagct ctactcgcca ctttttctca ttgttgctgc      604
tctagtattt ttaataacttt gcttcacat taagagaaag acagaatgaa tgagctcact      664
ttaattgact tctatctgtg ctttttagcc tttctgctat tccttgtttt aataatgctt      724
attatatttt ggttttcact cgaaatccag gatctagaag aaccttgtag caaagtctaa      784
acgaacatga aactttctcat tgttttgact tgtatttctc tatgcagttg catatgcact      844
gtagtacagc gctgtgcatc taataaacct catgtgcttg aagatccttg taaggtaaa      904
cactaggggt aataacttata gcactgcttg gctttgtgct ctaggaaagg ttttaccttt      964
tcatagatgg cacactatgg ttcaaacatg cacacctaag gttactatca actgtcaaga      1024
tccagctggg ggtgcgctta tagctaggtg ttggtacctt catgaaggtc accaaactgc      1084
tgcatttaga gacgtacttg ttgttttaaa taaacgaaca aattaaaatg tctgataatg      1144
gaccccaatc aaaccaacgt agtgccccc gcattacatt tgggtggacc acagattcaa      1204
ctgacaataa ccagaatgga ggacgca      1231

<210> 22
<211> 63
<212> PRT
<213> CORONAVIRUS

<400> 22
Met Phe His Leu Val Asp Phe Gln Val Thr Ile Ala Glu Ile Leu Ile
1       5       10       15
Ile Ile Met Arg Thr Phe Arg Ile Ala Ile Trp Asn Leu Asp Val Ile
       20       25       30
Ile Ser Ser Ile Val Arg Gln Leu Phe Lys Pro Leu Thr Lys Lys Asn
       35       40       45
Tyr Ser Glu Leu Asp Asp Glu Glu Pro Met Glu Leu Asp Tyr Pro
       50       55       60

<210> 23
<211> 1231
<212> DNA
<213> CORONAVIRUS

<220>
<221> CDS
<222> (285)..(650)
<223>

<400> 23
taccgtattg gaaactataa attaaataca gaccacgccg gtagcaacga caatattgct      60
ttgctagtagtac agtaagtgac aacagatggt tcatcttggt gacttccagg ttacaatagc      120
agagatattg attatcatta tgaggacttt caggattgct atttggaatc ttgacgttat      180
aataagttca atagtggagac aattatttaa gcctctaact aagaagaatt attcggagtt      240

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agatgatgaa gaacctatgg agttagatta tccataaaac gaac atg aaa att att 296
                                Met Lys Ile Ile
                                1
ctc ttc ctg aca ttg att gta ttt aca tct tgc gag cta tat cac tat 344
Leu Phe Leu Thr Leu Ile Val Phe Thr Ser Cys Glu Leu Tyr His Tyr
5                                10                                15                                20
cag gag tgt gtt aga ggt acg act gta cta cta aaa gaa cct tgc cca 392
Gln Glu Cys Val Arg Gly Thr Thr Val Leu Leu Lys Glu Pro Cys Pro
                                25                                30                                35
tca gga aca tac gag ggc aat tca cca ttt cac cct ctt gct gac aat 440
Ser Gly Thr Tyr Glu Gly Asn Ser Pro Phe His Pro Leu Ala Asp Asn
                                40                                45                                50
aaa ttt gca cta act tgc act agc aca cac ttt gct ttt gct tgt gct 488
Lys Phe Ala Leu Thr Cys Thr Ser Thr His Phe Ala Phe Ala Cys Ala
                                55                                60                                65
gac ggt act cga cat acc tat cag ctg cgt gca aga tca gtt tca cca 536
Asp Gly Thr Arg His Thr Tyr Gln Leu Arg Ala Arg Ser Val Ser Pro
                                70                                75                                80
aaa ctt ttc atc aga caa gag gag gtt caa caa gag ctc tac tcg cca 584
Lys Leu Phe Ile Arg Gln Glu Glu Val Gln Gln Glu Leu Tyr Ser Pro
85                                90                                95                                100
ctt ttt ctc att gtt gct gct cta gta ttt tta ata ctt tgc ttc acc 632
Leu Phe Leu Ile Val Ala Ala Leu Val Phe Leu Ile Leu Cys Phe Thr
                                105                                110                                115
att aag aga aag aca gaa tgaatgagct cactttaatt gacttctatt 680
Ile Lys Arg Lys Thr Glu
                                120
tgtgcttttt agcctttctg ctattccttg ttttaataat gcttattata ttttggtttt 740
cactcgaaat ccaggatcta gaagaacctt gtaccaaagt ctaaacgaac atgaaacttc 800
tcattgtttt gacttgattt tctctatgca gttgcatatg cactgtagta cagcgctgtg 860
catctaataa acctcatgtg cttgaagatc cttgtaaggt acaacactag gggtaatact 920
tatagcactg cttggctttg tgctctagga aagggttttac cttttcatag atggcacact 980
atgggttcaaa catgcacacc taatgttact atcaactgtc aagatccagc tgggtggtgcg 1040
cttatagcta ggtgttggtta ccttcatgaa ggtcacaaaa ctgctgcatt tagagacgta 1100
cttggtgttt taaataaacg aacaaattaa aatgtctgat aatggacccc aatcaaacca 1160
acgtagtgcc cccgcatta catttggtgg acccacagat tcaactgaca ataaccagaa 1220
tggaggacgc a 1231

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<210> 24
<211> 122
<212> PRT
<213> CORONAVIRUS

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<400> 24
Met Lys Ile Ile Leu Phe Leu Thr Leu Ile Val Phe Thr Ser Cys Glu
1                                5                                10                                15
Leu Tyr His Tyr Gln Glu Cys Val Arg Gly Thr Thr Val Leu Leu Lys
                                20                                25                                30
Glu Pro Cys Pro Ser Gly Thr Tyr Glu Gly Asn Ser Pro Phe His Pro
                                35                                40                                45
Leu Ala Asp Asn Lys Phe Ala Leu Thr Cys Thr Ser Thr His Phe Ala
50                                55                                60
Phe Ala Cys Ala Asp Gly Thr Arg His Thr Tyr Gln Leu Arg Ala Arg
65                                70                                75                                80
Ser Val Ser Pro Lys Leu Phe Ile Arg Gln Glu Glu Val Gln Gln Glu
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 5 10 15
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 Leu Val Leu Ile Met Leu Ile Ile Phe Trp Phe Ser Leu Glu Ile Gln
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 Asp Leu Glu Glu Pro Cys Thr Lys Val
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Met Cys Leu Lys Ile Leu

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30

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45

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 <211> 297
 <212> DNA
 <213> CORONAVIRUS

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aacttagatt	ccctcgaggc	cagggcggtc	caatcaacac	caatagtggg	ccagatgacc	240
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<210> 33
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 <213> CORONAVIRUS

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Gln Gly Gln Asn Ser Ala Asp Pro Lys Val Tyr Pro Ile Ile Leu Arg	
35 40 45	

Leu Gly Ser Gln Leu Ser Leu Ser Met Ala Arg Arg Asn Leu Asp Ser
 50 55 60
 Leu Glu Ala Arg Ala Phe Gln Ser Thr Pro Ile Val Val Gln Met Thr
 65 70 75 80
 Lys Leu Ala Thr Thr Glu Glu Leu Pro Asp Glu Phe Val Val Val Thr
 85 90 95
 Ala Lys

<210> 34
 <211> 213
 <212> DNA
 <213> CORONAVIRUS

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 caagaaattc aactcctggc agcagtaggg gaaattctcc tgctcgaatg gctagcggag 180
 gtgggtgaaac tgccctcgcg ctattgctgc tag 213

<210> 35
 <211> 70
 <212> PRT
 <213> CORONAVIRUS

<400> 35
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 20 25 30
 Pro His His Val Val Ala Val Ile Gln Glu Ile Gln Leu Leu Ala Ala
 35 40 45
 Val Gly Glu Ile Leu Leu Leu Glu Trp Leu Ala Glu Val Val Lys Leu
 50 55 60
 Pro Ser Arg Tyr Cys Cys
 65 70

<210> 36
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 <212> DNA
 <213> CORONAVIRUS

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<400> 36
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 Met Ser Asp Asn Gly Pro Gln Ser Asn Gln Arg Ser Ala Pro
 1 5 10
 cgc att aca ttt ggt gga ccc aca gat tca act gac aat aac cag aat 156
 Arg Ile Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn
 15 20 25 30
 gga gga cgc aat ggg gca agg cca aaa cag cgc cga ccc caa ggt tta 204
 Gly Gly Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu
 35 40 45
 ccc aat aat act gcg tct tgg ttc aca gct ctc act cag cat ggc aag 252
 Pro Asn Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys
 50 55 60

gag gaa ctt aga ttc cct cga ggc cag ggt cca atc aac acc aat	300
Glu Glu Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn	
65 70 75	
agt ggt cca gat gac caa att ggc tac tac cga aga gct acc cga cga	348
Ser Gly Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg	
80 85 90	
ggt cgt ggt ggt gac ggc aaa atg aaa gag ctc agc ccc aga tgg tac	396
Val Arg Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr	
95 100 105 110	
ttc tat tac cta gga act ggc cca gaa gct tca ctt ccc tac ggc gct	444
Phe Tyr Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala	
115 120 125	
aac aaa gaa ggc atc gta tgg gtt gca act gag gga gcc ttg aat aca	492
Asn Lys Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr	
130 135 140	
ccc aaa gac cac att ggc acc cgc aat cct aat aac aat gct gcc acc	540
Pro Lys Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr	
145 150 155	
gtg cta caa ctt cct caa gga aca aca ttg cca aaa ggc ttc tac gca	588
Val Leu Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala	
160 165 170	
gag gga agc aga ggc ggc agt caa gcc tct tct cgc tcc tca tca cgt	636
Glu Gly Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg	
175 180 185 190	
agt cgc ggt aat tca aga aat tca act cct ggc agc agt agg gga aat	684
Ser Arg Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn	
195 200 205	
tct cct gct cga atg gct agc gga ggt ggt gaa act gcc ctc gcg cta	732
Ser Pro Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu	
210 215 220	
ttg ctg cta gac aga ttg aac cag ctt gag agc aaa gtt tct ggt aaa	780
Leu Leu Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys	
225 230 235	
ggc caa caa caa caa ggc caa act gtc act aag aaa tct gct gct gag	828
Gly Gln Gln Gln Gln Gly Thr Val Thr Lys Lys Ser Ala Ala Glu	
240 245 250	
gca tct aaa aag cct cgc caa aaa cgt act gcc aca aaa cag tac aac	876
Ala Ser Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn	
255 260 265 270	
gtc act caa gca ttt ggg aga cgt ggt cca gaa caa acc caa gga aat	924
Val Thr Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn	
275 280 285	
ttc ggg gac caa gac cta atc aga caa gga act gat tac aaa cat tgg	972
Phe Gly Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp	
290 295 300	
ccg caa att gca caa ttt gct cca agt gcc tct gca ttc ttt gga atg	1020
Pro Gln Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met	
305 310 315	
tca cgc att ggc atg gaa gtc aca cct tcg gga aca tgg ctg act tat	1068
Ser Arg Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr	
320 325 330	
cat gga gcc att aaa ttg gat gac aaa gat cca caa ttc aaa gac aac	1116
His Gly Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn	
335 340 345 350	
gtc ata ctg ctg aac aag cac att gac gca tac aaa aca ttc cca cca	1164
Val Ile Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro	
355 360 365	
aca gag cct aaa aag gac aaa aag aaa aag act gat gaa gct cag cct	1212
Thr Glu Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro	
370 375 380	

ttg ccg cag aga caa aag aag cag ccc act gtg act ctt ctt cct gcg	1260
Leu Pro Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala	
385 390 395	
gct gac atg gat gat ttc tcc aga caa ctt caa aat tcc atg agt gga	1308
Ala Asp Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly	
400 405 410	
gct tct gct gat tca act cag gca taa acatcatga tgaccacaca	1355
Ala Ser Ala Asp Ser Thr Gln Ala	
415 420	
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<210> 37
 <211> 422
 <212> PRT
 <213> CORONAVIRUS

<400> 37

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Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn	
35 40 45	
Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu	
50 55 60	
Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly	
65 70 75 80	
Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg	
85 90 95	
Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr	
100 105 110	
Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys	
115 120 125	
Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys	
130 135 140	
Asp His Ile Gly Thr Arg Asn Pro Asn Asn Ala Ala Thr Val Leu	
145 150 155 160	
Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly	
165 170 175	
Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg	
180 185 190	
Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro	
195 200 205	
Ala Arg Met Ala Ser Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu	
210 215 220	
Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln	
225 230 235 240	
Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser	
245 250 255	
Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr	
260 265 270	
Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly	
275 280 285	
Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln	
290 295 300	
Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg	
305 310 315 320	
Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly	
325 330 335	
Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile	
340 345 350	

Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu
 355 360 365
 Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro
 370 375 380
 Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp
 385 390 395 400
 Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser
 405 410 415
 Ala Asp Ser Thr Gln Ala
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<210> 38
 <211> 1377
 <212> DNA
 <213> CORONAVIRUS

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 ggtggacca cagattcaac tgacaataac cagaatggag gacgcaatgg ggcaaggcca 180
 aaacagcgcc gacccaagg tttacccaat aatactgctt cttgggttcac agctctcact 240
 cagcatggca aggaggaact tagattccct cgaggccagg gcgttccaat caacaccaat 300
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 gccctcgctc tattgctgct agacagattg aaccagcttg agagcaaagt ttctggtaaa 780
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 gaagctcagc ctttgccgca gagacaaaag aagcagccca ctgtgactct tcttctcgct 1260
 gctgacatgg atgattttctc cagacaactt caaaattcca tgagtggagc ttctgctgat 1320
 tcaactcagg cataaacact catgatgacc acacaaggca gatgggctat gtaaacy 1377

<210> 39
 <211> 204
 <212> DNA
 <213> CORONAVIRUS

<400> 39
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 gcagtataaa caataataaa ttttactgtc gttgacaaga aacgagtaac tcgtccctct 180
 tctgcagact gcttacgggt tcgt 204

<210> 40
 <211> 809
 <212> DNA
 <213> CORONAVIRUS

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 gcctctgcat tctttggaat gtcacgcatt ggcattggaag tcacaccttc gggaacatgg 180
 ctgacttatc atggagccat taaattggat gacaaagatc cacaattcaa agacaacgtc 240

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aatctttaat	caatgtgtaa	cattagggag	gacttgaaag	agccaccaca	ttttcatcga	660
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tcttaggaga	atgacaaaaa	aaaaaaaaa				809

<210> 41
 <211> 448
 <212> DNA
 <213> CORONAVIRUS

<400> 41	
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acctaggtat	gctgatgatc gactgcaaca cggacgaaac cgtaagcagt ctgcagaaga 300
gggacgagtt	actcgtttct tgtcaacgac agtaaaattt attattgttt atactgcgta 360
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<210> 42
 <211> 2033
 <212> DNA
 <213> CORONAVIRUS

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 <211> 2018
 <212> DNA
 <213> CORONAVIRUS

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 <212> DNA
 <213> CORONAVIRUS

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<212> DNA

<213> CORONAVIRUS

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<210> 46

<211> 1995

<212> DNA

<213> CORONAVIRUS

<400> 46

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 <211> 1884
 <212> DNA
 <213> CORONAVIRUS

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<213> CORONAVIRUS

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<210> 49

<211> 2040

<212> DNA

<213> CORONAVIRUS

<400> 49

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<210> 50

<211> 2012

<212> DNA

<213> CORONAVIRUS

<400> 50

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<210> 51

<211> 1877

<212> DNA

<213> CORONAVIRUS

<400> 51

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<210> 52

<211> 2051

<212> DNA

<213> CORONAVIRUS

<400> 52

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<210> 53

<211> 2075

<212> DNA

<213> CORONAVIRUS

<400> 53

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<210> 54

<211> 1891

<212> DNA

<213> CORONAVIRUS

<400> 54

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Tyr	Val	Lys	Ser	Pro	Lys	Phe	Ser	Lys	Leu	Phe	Thr	Ile	Ala	Met
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Trp	Leu	Leu	Leu	Leu	Ser	Ile	Cys	Leu	Gly	Ser	Leu	Ile	Cys	Val
2210						2215					2220			
Thr	Ala	Ala	Phe	Gly	Val	Leu	Leu	Ser	Asn	Phe	Gly	Ala	Pro	Ser
2225						2230					2235			
Tyr	Cys	Asn	Gly	Val	Arg	Glu	Leu	Tyr	Leu	Asn	Ser	Ser	Asn	Val
2240						2245					2250			
Thr	Thr	Met	Asp	Phe	Cys	Glu	Gly	Ser	Phe	Pro	Cys	Ser	Ile	Cys
2255						2260					2265			
Leu	Ser	Gly	Leu	Asp	Ser	Leu	Asp	Ser	Tyr	Pro	Ala	Leu	Glu	Thr
2270						2275					2280			
Ile	Gln	Val	Thr	Ile	Ser	Ser	Tyr	Lys	Leu	Asp	Leu	Thr	Ile	Leu
2285						2290					2295			
Gly	Leu	Ala	Ala	Glu	Trp	Val	Leu	Ala	Tyr	Met	Leu	Phe	Thr	Lys
2300						2305					2310			
Phe	Phe	Tyr	Leu	Leu	Gly	Leu	Ser	Ala	Ile	Met	Gln	Val	Phe	Phe
2315						2320					2325			
Gly	Tyr	Phe	Ala	Ser	His	Phe	Ile	Ser	Asn	Ser	Trp	Leu	Met	Trp
2330						2335					2340			
Phe	Ile	Ile	Ser	Ile	Val	Gln	Met	Ala	Pro	Val	Ser	Ala	Met	Val
2345						2350					2355			
Arg	Met	Tyr	Ile	Phe	Phe	Ala	Ser	Phe	Tyr	Tyr	Ile	Trp	Lys	Ser
2360						2365					2370			
Tyr	Val	His	Ile	Met	Asp	Gly	Cys	Thr	Ser	Ser	Thr	Cys	Met	Met
2375						2380					2385			
Cys	Tyr	Lys	Arg	Asn	Arg	Ala	Thr	Arg	Val	Glu	Cys	Thr	Thr	Ile
2390						2395					2400			
Val	Asn	Gly	Met	Lys	Arg	Ser	Phe	Tyr	Val	Tyr	Ala	Asn	Gly	Gly
2405						2410					2415			
Arg	Gly	Phe	Cys	Lys	Thr	His	Asn	Trp	Asn	Cys	Leu	Asn	Cys	Asp
2420						2425					2430			
Thr	Phe	Cys	Thr	Gly	Ser	Thr	Phe	Ile	Ser	Asp	Glu	Val	Ala	Arg
2435						2440					2445			
Asp	Leu	Ser	Leu	Gln	Phe	Lys	Arg	Pro	Ile	Asn	Pro	Thr	Asp	Gln
2450						2455					2460			
Ser	Ser	Tyr	Ile	Val	Asp	Ser	Val	Ala	Val	Lys	Asn	Gly	Ala	Leu
2465						2470					2475			
His	Leu	Tyr	Phe	Asp	Lys	Ala	Gly	Gln	Lys	Thr	Tyr	Glu	Arg	His
2480						2485					2490			

Pro	Leu	Ser	His	Phe	Val	Asn	Leu	Asp	Asn	Leu	Arg	Ala	Asn	Asn	
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Thr	Lys	Gly	Ser	Leu	Pro	Ile	Asn	Val	Ile	Val	Phe	Asp	Gly	Lys	
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Ser	Lys	Cys	Asp	Glu	Ser	Ala	Ser	Lys	Ser	Ala	Ser	Val	Tyr	Tyr	
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Ser	Gln	Leu	Met	Cys	Gln	Pro	Ile	Leu	Leu	Leu	Asp	Gln	Ala	Leu	
	2540					2545					2550				
Val	Ser	Asp	Val	Gly	Asp	Ser	Thr	Glu	Val	Ser	Val	Lys	Met	Phe	
	2555					2560					2565				
Asp	Ala	Tyr	Val	Asp	Thr	Phe	Ser	Ala	Thr	Phe	Ser	Val	Pro	Met	
	2570					2575					2580				
Glu	Lys	Leu	Lys	Ala	Leu	Val	Ala	Thr	Ala	His	Ser	Glu	Leu	Ala	
	2585					2590					2595				
Lys	Gly	Val	Ala	Leu	Asp	Gly	Val	Leu	Ser	Thr	Phe	Val	Ser	Ala	
	2600					2605					2610				
Ala	Arg	Gln	Gly	Val	Val	Asp	Thr	Asp	Val	Asp	Thr	Lys	Asp	Val	
	2615					2620					2625				
Ile	Glu	Cys	Leu	Lys	Leu	Ser	His	His	Ser	Asp	Leu	Glu	Val	Thr	
	2630					2635					2640				
Gly	Asp	Ser	Cys	Asn	Asn	Phe	Met	Leu	Thr	Tyr	Asn	Lys	Val	Glu	
	2645					2650					2655				
Asn	Met	Thr	Pro	Arg	Asp	Leu	Gly	Ala	Cys	Ile	Asp	Cys	Asn	Ala	
	2660					2665					2670				
Arg	His	Ile	Asn	Ala	Gln	Val	Ala	Lys	Ser	His	Asn	Val	Ser	Leu	
	2675					2680					2685				
Ile	Trp	Asn	Val	Lys	Asp	Tyr	Met	Ser	Leu	Ser	Glu	Gln	Leu	Arg	
	2690					2695					2700				
Lys	Gln	Ile	Arg	Ser	Ala	Ala	Lys	Lys	Asn	Asn	Ile	Pro	Phe	Arg	
	2705					2710					2715				
Leu	Thr	Cys	Ala	Thr	Thr	Arg	Gln	Val	Val	Asn	Val	Ile	Thr	Thr	
	2720					2725					2730				
Lys	Ile	Ser	Leu	Lys	Gly	Gly	Lys	Ile	Val	Ser	Thr	Cys	Phe	Lys	
	2735					2740					2745				
Leu	Met	Leu	Lys	Ala	Thr	Leu	Leu	Cys	Val	Leu	Ala	Ala	Leu	Val	
	2750					2755					2760				
Cys	Tyr	Ile	Val	Met	Pro	Val	His	Thr	Leu	Ser	Ile	His	Asp	Gly	
	2765					2770					2775				
Tyr	Thr	Asn	Glu	Ile	Ile	Gly	Tyr	Lys	Ala	Ile	Gln	Asp	Gly	Val	
	2780					2785					2790				
Thr	Arg	Asp	Ile	Ile	Ser	Thr	Asp	Asp	Cys	Phe	Ala	Asn	Lys	His	
	2795					2800					2805				
Ala	Gly	Phe	Asp	Ala	Trp	Phe	Ser	Gln	Arg	Gly	Gly	Ser	Tyr	Lys	
	2810					2815					2820				
Asn	Asp	Lys	Ser	Cys	Pro	Val	Val	Ala	Ala	Ile	Ile	Thr	Arg	Glu	
	2825					2830					2835				
Ile	Gly	Phe	Ile	Val	Pro	Gly	Leu	Pro	Gly	Thr	Val	Leu	Arg	Ala	
	2840					2845					2850				
Ile	Asn	Gly	Asp	Phe	Leu	His	Phe	Leu	Pro	Arg	Val	Phe	Ser	Ala	
	2855					2860					2865				
Val	Gly	Asn	Ile	Cys	Tyr	Thr	Pro	Ser	Lys	Leu	Ile	Glu	Tyr	Ser	
	2870					2875					2880				
Asp	Phe	Ala	Thr	Ser	Ala	Cys	Val	Leu	Ala	Ala	Glu	Cys	Thr	Ile	
	2885					2890					2895				
Phe	Lys	Asp	Ala	Met	Gly	Lys	Pro	Val	Pro	Tyr	Cys	Tyr	Asp	Thr	
	2900					2905					2910				
Asn	Leu	Leu	Glu	Gly	Ser	Ile	Ser	Tyr	Ser	Glu	Leu	Arg	Pro	Asp	
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Thr	Arg	Tyr	Val	Leu	Met	Asp	Gly	Ser	Ile	Ile	Gln	Phe	Pro	Asn	
	2930					2935					2940				
Thr	Tyr	Leu	Glu	Gly	Ser	Val	Arg	Val	Val	Thr	Thr	Phe	Asp	Ala	
	2945					2950					2955				

Glu Tyr Cys Arg His Gly Thr Cys Glu Arg Ser Glu Val Gly Ile	2960	2965	2970
Cys Leu Ser Thr Ser Gly Arg Trp Val Leu Asn Asn Glu His Tyr	2975	2980	2985
Arg Ala Leu Ser Gly Val Phe Cys Gly Val Asp Ala Met Asn Leu	2990	2995	3000
Ile Ala Asn Ile Phe Thr Pro Leu Val Gln Pro Val Gly Ala Leu	3005	3010	3015
Asp Val Ser Ala Ser Val Val Ala Gly Gly Ile Ile Ala Ile Leu	3020	3025	3030
Val Thr Cys Ala Ala Tyr Tyr Phe Met Lys Phe Arg Arg Val Phe	3035	3040	3045
Gly Glu Tyr Asn His Val Val Ala Ala Asn Ala Leu Leu Phe Leu	3050	3055	3060
Met Ser Phe Thr Ile Leu Cys Leu Val Pro Ala Tyr Ser Phe Leu	3065	3070	3075
Pro Gly Val Tyr Ser Val Phe Tyr Leu Tyr Leu Thr Phe Tyr Phe	3080	3085	3090
Thr Asn Asp Val Ser Phe Leu Ala His Leu Gln Trp Phe Ala Met	3095	3100	3105
Phe Ser Pro Ile Val Pro Phe Trp Ile Thr Ala Ile Tyr Val Phe	3110	3115	3120
Cys Ile Ser Leu Lys His Cys His Trp Phe Phe Asn Asn Tyr Leu	3125	3130	3135
Arg Lys Arg Val Met Phe Asn Gly Val Thr Phe Ser Thr Phe Glu	3140	3145	3150
Glu Ala Ala Leu Cys Thr Phe Leu Leu Asn Lys Glu Met Tyr Leu	3155	3160	3165
Lys Leu Arg Ser Glu Thr Leu Leu Pro Leu Thr Gln Tyr Asn Arg	3170	3175	3180
Tyr Leu Ala Leu Tyr Asn Lys Tyr Lys Tyr Phe Ser Gly Ala Leu	3185	3190	3195
Asp Thr Thr Ser Tyr Arg Glu Ala Ala Cys Cys His Leu Ala Lys	3200	3205	3210
Ala Leu Asn Asp Phe Ser Asn Ser Gly Ala Asp Val Leu Tyr Gln	3215	3220	3225
Pro Pro Gln Thr Ser Ile Thr Ser Ala Val Leu Gln Ser Gly Phe	3230	3235	3240
Arg Lys Met Ala Phe Pro Ser Gly Lys Val Glu Gly Cys Met Val	3245	3250	3255
Gln Val Thr Cys Gly Thr Thr Thr Leu Asn Gly Leu Trp Leu Asp	3260	3265	3270
Asp Thr Val Tyr Cys Pro Arg His Val Ile Cys Thr Ala Glu Asp	3275	3280	3285
Met Leu Asn Pro Asn Tyr Glu Asp Leu Leu Ile Arg Lys Ser Asn	3290	3295	3300
His Ser Phe Leu Val Gln Ala Gly Asn Val Gln Leu Arg Val Ile	3305	3310	3315
Gly His Ser Met Gln Asn Cys Leu Leu Arg Leu Lys Val Asp Thr	3320	3325	3330
Ser Asn Pro Lys Thr Pro Lys Tyr Lys Phe Val Arg Ile Gln Pro	3335	3340	3345
Gly Gln Thr Phe Ser Val Leu Ala Cys Tyr Asn Gly Ser Pro Ser	3350	3355	3360
Gly Val Tyr Gln Cys Ala Met Arg Pro Asn His Thr Ile Lys Gly	3365	3370	3375
Ser Phe Leu Asn Gly Ser Cys Gly Ser Val Gly Phe Asn Ile Asp	3380	3385	3390
Tyr Asp Cys Val Ser Phe Cys Tyr Met His His Met Glu Leu Pro	3395	3400	3405
Thr Gly Val His Ala Gly Thr Asp Leu Glu Gly Lys Phe Tyr Gly	3410	3415	3420

Pro	Phe	Val	Asp	Arg	Gln	Thr	Ala	Gln	Ala	Ala	Gly	Thr	Asp	Thr
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Thr	Ile	Thr	Leu	Asn	Val	Leu	Ala	Trp	Leu	Tyr	Ala	Ala	Val	Ile
	3440					3445					3450			
Asn	Gly	Asp	Arg	Trp	Phe	Leu	Asn	Arg	Phe	Thr	Thr	Thr	Leu	Asn
	3455					3460					3465			
Asp	Phe	Asn	Leu	Val	Ala	Met	Lys	Tyr	Asn	Tyr	Glu	Pro	Leu	Thr
	3470					3475					3480			
Gln	Asp	His	Val	Asp	Ile	Leu	Gly	Pro	Leu	Ser	Ala	Gln	Thr	Gly
	3485					3490					3495			
Ile	Ala	Val	Leu	Asp	Met	Cys	Ala	Ala	Leu	Lys	Glu	Leu	Leu	Gln
	3500					3505					3510			
Asn	Gly	Met	Asn	Gly	Arg	Thr	Ile	Leu	Gly	Ser	Thr	Ile	Leu	Glu
	3515					3520					3525			
Asp	Glu	Phe	Thr	Pro	Phe	Asp	Val	Val	Arg	Gln	Cys	Ser	Gly	Val
	3530					3535					3540			
Thr	Phe	Gln	Gly	Lys	Phe	Lys	Lys	Ile	Val	Lys	Gly	Thr	His	His
	3545					3550					3555			
Trp	Met	Leu	Leu	Thr	Phe	Leu	Thr	Ser	Leu	Leu	Ile	Leu	Val	Gln
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Ser	Thr	Gln	Trp	Ser	Leu	Phe	Phe	Phe	Val	Tyr	Glu	Asn	Ala	Phe
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	3605					3610					3615			
Pro	Ser	Leu	Ala	Thr	Val	Ala	Tyr	Phe	Asn	Met	Val	Tyr	Met	Pro
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Ala	Ser	Trp	Val	Met	Arg	Ile	Met	Thr	Trp	Leu	Glu	Leu	Ala	Asp
	3635					3640					3645			
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Cys	Thr	Ser	Val	Val	Leu	Leu	Ser	Val	Leu	Gln	Gln	Leu	Arg	Val
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Glu	Ser	Ser	Ser	Lys	Leu	Trp	Ala	Gln	Cys	Val	Gln	Leu	His	Asn
	3860					3865					3870			
Asp	Ile	Leu	Leu	Ala	Lys	Asp	Thr	Thr	Glu	Ala	Phe	Glu	Lys	Met
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Val	Ser	Leu	Leu	Ser	Val	Leu	Leu	Ser	Met	Gln	Gly	Ala	Val	Asp
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Ile	Asn	Arg	Leu	Cys	Glu	Glu	Met	Leu	Asp	Asn	Arg	Ala	Thr	Leu
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Gln	Ala	Ile	Ala	Ser	Glu	Phe	Ser	Ser	Leu	Pro	Ser	Tyr	Ala	Ala
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Tyr	Ala	Thr	Ala	Gln	Glu	Ala	Tyr	Glu	Gln	Ala	Val	Ala	Asn	Gly
3935						3940					3945			
Asp	Ser	Glu	Val	Val	Leu	Lys	Lys	Leu	Lys	Lys	Ser	Leu	Asn	Val
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Ala	Lys	Ser	Glu	Phe	Asp	Arg	Asp	Ala	Ala	Met	Gln	Arg	Lys	Leu
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Glu	Lys	Met	Ala	Asp	Gln	Ala	Met	Thr	Gln	Met	Tyr	Lys	Gln	Ala
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Val	Lys	Leu	Gln	Asn	Asn	Glu	Leu	Ser	Pro	Val	Ala	Leu	Arg	Gln
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Pro	Lys	Ser	Asp	Gly	Thr	Gly	Thr	Ile	Tyr	Thr	Glu	Leu	Glu	Pro
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Pro	Cys	Arg	Phe	Val	Thr	Asp	Thr	Pro	Lys	Gly	Pro	Lys	Val	Lys
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Tyr	Leu	Tyr	Phe	Ile	Lys	Gly	Leu	Asn	Asn	Leu	Asn	Arg	Gly	Met
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Phe	Ala	Val	Asp	Pro	Ala	Lys	Ala	Tyr	Lys	Asp	Tyr	Leu	Ala	Ser
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Gly	Gly	Gln	Pro	Ile	Thr	Asn	Cys	Val	Lys	Met	Leu	Cys	Thr	His
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Gly	Phe	Thr	Leu	Arg	Asn	Thr	Val	Cys	Thr	Val	Cys	Gly	Met	Trp
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 Gln Ser Ala Asp Ala Ser Thr Phe Leu Asn Gly Phe Ala Val
 4370 4375 4380

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 Thr Ser Thr Asp Val Val Tyr Arg Ala Phe Asp Ile Tyr Asn Glu Lys
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 Val Ala Gly Phe Ala Lys Phe Leu Lys Thr Asn Cys Cys Arg Phe Gln
 35 40 45
 Glu Lys Asp Glu Glu Gly Asn Tyr Gln His Glu Glu Thr Ile Tyr Asn Leu
 50 55 60
 Arg His Thr Met Ser Asn Tyr Gln His Glu Glu Thr Ile Tyr Asn Leu
 65 70 75 80
 Val Lys Asp Cys Pro Ala Val Ala Val His Asp Phe Phe Lys Phe Arg
 85 90 95
 Val Asp Gly Asp Met Val Pro His Ile Ser Arg Gln Arg Leu Thr Lys
 100 105 110
 Tyr Thr Met Ala Asp Leu Val Tyr Ala Leu Arg His Phe Asp Glu Gly
 115 120 125
 Asn Cys Asp Thr Leu Lys Glu Ile Leu Val Thr Tyr Asn Cys Cys Asp
 130 135 140
 Asp Asp Tyr Phe Asn Lys Lys Asp Trp Tyr Asp Phe Val Glu Asn Pro
 145 150 155 160
 Asp Ile Leu Arg Val Tyr Ala Asn Leu Gly Glu Arg Val Arg Gln Ser
 165 170 175
 Leu Leu Lys Thr Val Gln Phe Cys Asp Ala Met Arg Asp Ala Gly Ile
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 Val Gly Val Leu Thr Leu Asp Asn Gln Asp Leu Asn Gly Asn Trp Tyr
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 Asp Phe Gly Asp Phe Val Gln Val Ala Pro Gly Cys Gly Val Pro Ile
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 Val Asp Ser Tyr Tyr Ser Leu Leu Met Pro Ile Leu Thr Leu Thr Arg
 225 230 235 240
 Ala Leu Ala Ala Glu Ser His Met Asp Ala Asp Leu Ala Lys Pro Leu
 245 250 255
 Ile Lys Trp Asp Leu Leu Lys Tyr Asp Phe Thr Glu Glu Arg Leu Cys
 260 265 270
 Leu Phe Asp Arg Tyr Phe Lys Tyr Trp Asp Gln Thr Tyr His Pro Asn
 275 280 285
 Cys Ile Asn Cys Leu Asp Asp Arg Cys Ile Leu His Cys Ala Asn Phe
 290 295 300
 Asn Val Leu Phe Ser Thr Val Phe Pro Pro Thr Ser Phe Gly Pro Leu
 305 310 315 320
 Val Arg Lys Ile Phe Val Asp Gly Val Pro Phe Val Val Ser Thr Gly
 325 330 335
 Tyr His Phe Arg Glu Leu Gly Val Val His Asn Gln Asp Val Asn Leu
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 His Ser Ser Arg Leu Ser Phe Lys Glu Leu Leu Val Tyr Ala Ala Asp
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 Pro Ala Met His Ala Ala Ser Gly Asn Leu Leu Leu Asp Lys Arg Thr
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64															
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Lys	Gly	Phe	Phe	Lys	Glu	Gly	Ser	Ser	Val	Glu	Leu	Lys	His	Phe	Phe
			420					425					430		
Phe	Ala	Gln	Asp	Gly	Asn	Ala	Ala	Ile	Ser	Asp	Tyr	Asp	Tyr	Tyr	Arg
		435					440					445			
Tyr	Asn	Leu	Pro	Thr	Met	Cys	Asp	Ile	Arg	Gln	Leu	Leu	Phe	Val	Val
	450					455					460				
Glu	Val	Val	Asp	Lys	Tyr	Phe	Asp	Cys	Tyr	Asp	Gly	Gly	Cys	Ile	Asn
465					470					475					480
Ala	Asn	Gln	Val	Ile	Val	Asn	Asn	Leu	Asp	Lys	Ser	Ala	Gly	Phe	Pro
				485					490					495	
Phe	Asn	Lys	Trp	Gly	Lys	Ala	Arg	Leu	Tyr	Tyr	Asp	Ser	Met	Ser	Tyr
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Glu	Asp	Gln	Asp	Ala	Leu	Phe	Ala	Tyr	Thr	Lys	Arg	Asn	Val	Ile	Pro
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Thr	Ile	Thr	Gln	Met	Asn	Leu	Lys	Tyr	Ala	Ile	Ser	Ala	Lys	Asn	Arg
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Gln	Phe	His	Gln	Lys	Leu	Leu	Lys	Ser	Ile	Ala	Ala	Thr	Arg	Gly	Ala
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Thr	Val	Val	Ile	Gly	Thr	Ser	Lys	Phe	Tyr	Gly	Gly	Trp	His	Asn	Met
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Asp	Tyr	Pro	Lys	Cys	Asp	Arg	Ala	Met	Pro	Asn	Met	Leu	Arg	Ile	Met
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His	Arg	Phe	Tyr	Arg	Leu	Ala	Asn	Glu	Cys	Ala	Gln	Val	Leu	Ser	Glu
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Met	Val	Met	Cys	Gly	Gly	Ser	Leu	Tyr	Val	Lys	Pro	Gly	Gly	Thr	Ser
			660					665					670		
Ser	Gly	Asp	Ala	Thr	Thr	Ala	Tyr	Ala	Asn	Ser	Val	Phe	Asn	Ile	Cys
	675						680					685			
Gln	Ala	Val	Thr	Ala	Asn	Val	Asn	Ala	Leu	Leu	Ser	Thr	Asp	Gly	Asn
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Lys	Ile	Ala	Asp	Lys	Tyr	Val	Arg	Asn	Leu	Gln	His	Arg	Leu	Tyr	Glu
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Cys	Leu	Tyr	Arg	Asn	Arg	Asp	Val	Asp	His	Glu	Phe	Val	Asp	Glu	Phe
				725					730					735	
Tyr	Ala	Tyr	Leu	Arg	Lys	His	Phe	Ser	Met	Met	Ile	Leu	Ser	Asp	Asp
			740					745					750		
Ala	Val	Val	Cys	Tyr	Asn	Ser	Asn	Tyr	Ala	Ala	Gln	Gly	Leu	Val	Ala
	755						760					765			
Ser	Ile	Lys	Asn	Phe	Lys	Ala	Val	Leu	Tyr	Tyr	Gln	Asn	Asn	Val	Phe
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Met	Ser	Glu	Ala	Lys	Cys	Trp	Thr	Glu	Thr	Asp	Leu	Thr	Lys	Gly	Pro
785					790					795					800
His	Glu	Phe	Cys	Ser	Gln	His	Thr	Met	Leu	Val	Lys	Gln	Gly	Asp	Asp
			805						810					815	
Tyr	Val	Tyr	Leu	Pro	Tyr	Pro	Asp	Pro	Ser	Arg	Ile	Leu	Gly	Ala	Gly
			820					825					830		
Cys	Phe	Val	Asp	Asp	Ile	Val	Lys	Thr	Asp	Gly	Thr	Leu	Met	Ile	Glu
	835						840					845			
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	850					855					860				
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865					870					875					880
Lys	Leu	His	Asp	Glu	Leu	Thr	Gly	His	Met	Leu	Asp	Met	Tyr	Ser	Val
				885					890					895	

Met	Leu	Thr	Asn	Asp	Asn	Thr	Ser	Arg	Tyr	Trp	Glu	Pro	Glu	Phe	Tyr	900	905	910
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Val	Leu	Cys	Asn	Ser	Gln	Thr	Ser	Leu	Arg	Cys	Gly	Ala	Cys	Ile	Arg	930	935	940
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Ser	His	Lys	Leu	Val	Leu	Ser	Val	Asn	Pro	Tyr	Val	Cys	Asn	Ala	Pro	965	970	975
Gly	Cys	Asp	Val	Thr	Asp	Val	Thr	Gln	Leu	Tyr	Leu	Gly	Gly	Met	Ser	980	985	990
Tyr	Tyr	Cys	Lys	Ser	His	Lys	Pro	Pro	Ile	Ser	Phe	Pro	Leu	Cys	Ala	995	1000	1005
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Lys	Leu	Phe	Ala	Ala	Glu	Thr	Leu	Lys	Ala	Thr	Glu	Glu	Thr	Phe		1055	1060	1065
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Arg	Glu	Leu	His	Leu	Ser	Trp	Glu	Val	Gly	Lys	Pro	Arg	Pro	Pro		1085	1090	1095
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Pro	Ile	Asp	Lys	Cys	Ser	Arg	Ile	Ile	Pro	Ala	Arg	Ala	Arg	Val		1250	1255	1260
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Val	Phe	Cys	Thr	Val	Asn	Ala	Leu	Pro	Glu	Thr	Thr	Ala	Asp	Ile		1280	1285	1290
Val	Val	Phe	Asp	Glu	Ile	Ser	Met	Ala	Thr	Asn	Tyr	Asp	Leu	Ser		1295	1300	1305
Val	Val	Asn	Ala	Arg	Leu	Arg	Ala	Lys	His	Tyr	Val	Tyr	Ile	Gly		1310	1315	1320
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Thr	Leu	Glu	Pro	Glu	Tyr	Phe	Asn	Ser	Val	Cys	Arg	Leu	Met	Lys		1340	1345	1350
Thr	Ile	Gly	Pro	Asp	Met	Phe	Leu	Gly	Thr	Cys	Arg	Arg	Cys	Pro		1355	1360	1365

Ala	Glu	Ile	Val	Asp	Thr	Val	Ser	Ala	Leu	Val	Tyr	Asp	Asn	Lys
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Leu	Lys	Ala	His	Lys	Asp	Lys	Ser	Ala	Gln	Cys	Phe	Lys	Met	Phe
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Tyr	Lys	Gly	Val	Ile	Thr	His	Asp	Val	Ser	Ser	Ala	Ile	Asn	Arg
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Pro	Gln	Ile	Gly	Val	Val	Arg	Glu	Phe	Leu	Thr	Arg	Asn	Pro	Ala
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Trp	Arg	Lys	Ala	Val	Phe	Ile	Ser	Pro	Tyr	Asn	Ser	Gln	Asn	Ala
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Thr	Arg	Ala	Lys	Ile	Gly	Ile	Leu	Cys	Ile	Met	Ser	Asp	Arg	Asp
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Pro	Asn	Met	Phe	Ile	Thr	Arg	Glu	Glu	Ala	Ile	Arg	His	Val	Arg
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Ala	Phe	Asp	Lys	Ser	Ala	Phe	Thr	Asn	Leu	Lys	Gln	Leu	Pro	Phe
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Glu	His	Ile	Val	Tyr	Gly	Asp	Phe	Ser	His	Gly	Gln	Leu	Gly	Gly
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cagaccaagt	ttactcatat	atactttaga	ttgattttaa	acttcatttt	taatttataa	7020
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<220>

<223> SNE-S1 primer

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23

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<212> DNA

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<223> SNE-AS1 primer

<400> 142

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24

<210> 143

<211> 21

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<210> 148
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<223> N-terminal end of SRAS-CoV S protein (amino acids 1 to 13)

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1 5 10

<210> 150

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<212> PRT

<213> Artificial sequence

<220>

<223> oligopeptide

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Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys
1 5 10

<210> 151

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<223> PCR primer

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34

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<211> 33

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<223> PCR primer

<400> 152

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33

<210> 153

<211> 59

<212> DNA

<213> Artificial sequence

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<223> oligonucleotid

<400> 153

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59

<210> 154

<211> 53

<212> DNA

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<210> 155
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<220>
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